

## **AMENDMENT TO THE CLAIMS**

Please amend the claims as shown below. The listing of claims below will replace all prior versions of claims in this application.

1. (Currently Amended) A method for detecting for the presence of antibiotic resistant *Staphylococcus* bacteria from total unamplified *Staphylococcus* genomic DNA in a sample, the sample comprising a wild-type *mecA* gene sequence or fragment thereof, one or more mutant *mecA* gene sequence or fragment thereof which differ from the wild-type *mecA* gene sequence by at least one nucleotide, or both,~~detecting for the presence or absence of one or more target nucleic acid sequences in a sample, wherein the sample comprises nucleic acid molecules of higher biological complexity relative to amplified nucleic acid molecules and wherein the sample comprises a wild-type target nucleic acid sequence, one or more mutant target nucleic acid sequences which differ from a wild-type target nucleic acid sequence by at least one nucleotide, or both,~~ the method comprising the steps of:

- a) providing an addressable substrate having bound thereto (i) wild-type capture oligonucleotides bound thereto, wherein the wild-type capture oligonucleotides comprise a wild-type capture oligonucleotide having a sequence that is complementary to at least part of a first portion of the wild-type *mecA* gene sequence or fragment thereof, and (ii) one or more mutant capture oligonucleotides having a sequence that is complementary to at least part of a first portion of the mutant *mecA* gene sequence or fragment thereof~~the wild-type target nucleic acid sequence and one or more different mutant capture oligonucleotides, wherein each mutant capture oligonucleotide has a sequence that is complementary to at least part of the first portion of a specific mutant target nucleic acid sequence;~~
- b) providing a detection probe comprising detector oligonucleotides bound to a gold nanoparticle, wherein the detector oligonucleotides have a sequence that is complementary to at least part of a second portion of the *mecA* gene sequence or fragment thereof~~target nucleic acid sequence of step (a);~~
- c) contacting the sample with the substrate and the detection probe under conditions that are effective for (i) the hybridization of the capture oligonucleotides to the first portion of the *mecA* gene sequence or fragment thereof,~~target nucleic acid sequence and (ii) the hybridization of the detection probe to the second portion of the *mecA* gene sequence or~~

~~fragment thereof, target nucleic acid sequence and (iii) the to allow for discrimination between the wild-type mecA gene sequence or fragment thereof target nucleic acid and said one or more mutant mecA gene sequence or fragment thereof target nucleic acid sequences that differ by at least one nucleotide; and~~

- d) detecting whether the capture oligonucleotide and detection probe hybridized with the first and second portions of the mecA gene sequence or fragment thereof target nucleic acid sequence.

2. (Currently Amended) The method of claim 1, wherein the mecA gene sequence or fragment thereof target nucleic acid sequence comprises a Single Nucleotide Polymorphism.

3. (Original) The method of claim 1, wherein the single nucleotide difference is recognized by the capture oligonucleotide bound to the substrate.

4. (Original) The method of claim 1, wherein the single nucleotide difference is recognized by the detector oligonucleotides.

5. (Cancelled)

6. (Original) The method of claim 1, wherein the substrate comprises a plurality of capture oligonucleotides, each of which can recognize a different single nucleotide polymorphism.

7. (Currently Amended) The method of claim 1, wherein the sample comprises more than one mecA gene sequence or fragment thereof nucleic acid target, each of which comprises one or more different single nucleotide polymorphisms.

8. (Currently Amended) The method of claim 1, wherein one or more types of detector probes are provided, each of which has detector oligonucleotides bound thereto that are capable of hybridizing to the mecA gene sequence or fragment thereof with a different nucleic acid target.

9. (Withdrawn) The method of claim 1, wherein sample is contacted with the

detector probe so that a nucleic acid target present in the sample hybridizes with the detector oligonucleotides on the detector probe, and the nucleic acid target bound to the detector probe is then contacted with the substrate so that the nucleic acid target hybridizes with the capture oligonucleotide on the substrate.

10. (Currently Amended) The method of claim 1, wherein sample is contacted with the substrate so that the mecA gene sequence or fragment thereof~~a nucleic acid target~~ present in the sample hybridizes with the~~a~~ capture oligonucleotide, and the mecA gene sequence or fragment thereof~~nucleic acid target~~ bound to the capture oligonucleotide is then contacted with the detector probe so that the mecA gene sequence or fragment thereof~~nucleic acid target~~ hybridizes with the detector oligonucleotides on the detector probe.

11. (Withdrawn) The method of claim 1, wherein the sample is contacted simultaneously with the detector probe and the substrate.

12. (Cancelled)

13. (Currently Amended) The method of claim 1~~claim 12~~, wherein the detection probelabel allows detection by photonic, electronic, acoustic, opto-acoustic, gravity, electro-chemical, electro-optic, mass-spectrometric, enzymatic, chemical, biochemical, or physical means.

14. (Withdrawn-Currently Amended) The method of claim 1~~12~~, wherein the label is fluorescent, luminescent, phosphorescent, radioactive, nanoparticle, dendrimer, molecular aggregate, quantum dot, or a bead.

15. to 26. (Cancelled)

27. (Currently Amended) The method of claim 123, wherein the detecting comprises contacting the substrate with silver stain.

28. (Currently Amended) The method of claim 123, wherein the detecting comprises detecting light scattered by the nanoparticle.

29. (Currently Amended) The method of claim 123, wherein the detecting comprises observation with an optical scanner.

30. (Currently Amended) The method of claim 123, wherein the detecting comprises observation with a flatbed scanner.

31. (Original) The method of claim 29 or 30, wherein the scanner is linked to a computer loaded with software capable of calculating grayscale measurements, and the grayscale measurements are calculated to provide a quantitative measure of the amount of nucleic acid detected.

32. (Currently Amended) The method of claim 123, wherein the oligonucleotides attached to the substrate are located between two electrodes, the nanoparticles are made of a material that is a conductor of electricity, and step (d) comprises detecting a change in conductivity.

33. (Original) The method of claim 32, wherein the electrodes are made of gold and the nanoparticles are made of gold.

34. (Original) The method of claim 32, wherein the substrate is contacted with silver stain to produce the change in conductivity.

35. (Currently Amended) The method of claims 123, wherein a plurality of capture oligonucleotides, each of which can recognize a different mecA gene sequence or fragment thereof~~target nucleic acid sequence~~, are attached to the substrate in an array of spots and each spot of oligonucleotides is located between two electrodes, the nanoparticles are made of a material that is a conductor of electricity, and step (d) comprises detecting a change in conductivity.

36. (Original) The method of claim 35, wherein the electrodes are made of gold and the nanoparticles are made of gold.

37. (Original) The method of claim 35, wherein the substrate is contacted with silver stain to produce the change in conductivity.

38. to 162. (Cancelled)

163. (Withdrawn) The method of claim 1, wherein at least one of the target nucleic acid sequences is a portion of a gene of a Staphylococcus bacterium and at least one of the target nucleic acid sequences is a portion of the mecA gene.

164.-167. (Cancelled)

168. (New) The method of claim 1, wherein the substrate further comprises one or more capture oligonucleotides having sequences that are complementary to Tuf gene, 16S rRNA gene, or both, or to fragments thereof.

169. (New) The method of claim 168, wherein the method is used to distinguish between two or more species of a common genus.

170. (New) The method of claim 169, wherein the species differ by two or more non-consecutive nucleotides.

171. (New) The method of claim 169, wherein the species differ by two or more consecutive nucleotides.

172. (New) The method of claim 169, wherein the species differ by at least one nucleotide.